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Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
 You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: aan54413, (226 residues) AAN54413 vs SEQ ID NO:4
 Sequence 2: seq (226 residues) SEQ ID NO:4

using the parameters:

Comparison matrix: BLOSUM62
 Number of alignments computed: 20
 Gap open penalty: 12
 Gap extension penalty: 4

 Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

85.4% identity in 226 residues overlap; Score: 1012.0; Gap frequency: 0.0%

```

aan54413,      1 MEPIKNLPRLCRTLGYEFKNLDLLTQALHRSAAANKHNERLEFLGDSILSIVISDALYHQ
seq            1 MEPIKNLPRLCRTLGYEFNNIELLIQALHRSAAANKHNERLEFLGDSILSIAISDALYHQ
                ***** *  ** *****

aan54413,      61 FPKATEGDLSRMRATLVRGDTLTLLIAQAFKLG DYLFLGPGELKSGGFRRESILADAVEAI
seq            61 FPKATEGDLSRMRATLVKGDTLTIIAKEFKLG DYLYLGPGLKSGGFRRESILADAVEAI
                ***** *  *****

aan54413,      121 IGAIYLDSDLEVC RQLLLN WYAERLAEIQPGINQKDAKTL LQEYLQGLKKPLPDYQVINI
seq            121 IGAVYLDADIEVC RKL LLSWYQERLAEIKPGINQKDPKTI LQEYLQGFKKPLPDYQVVAV
                *** * * * * * * * * * * * * * * * * * * * * * * * * * * * *

aan54413,      181 EGD AHDQTFTVECRIDDL SQSVIGVASSRRKAEQIAAAQVLELLKK
seq            181 EGE AHDQTFTVECKISELDKVV TGVASSRRKAEQLAAQVLELLNK
                ** ***** *  *  *****

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